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CLAIMS

1. Method for inducing resistance to a group I virus comprising a TGB2 sequence in a plant cell or a plant, comprising the following steps:

- preparing a nucleotide construct comprising a nucleotide sequence having at least 70% homology with the nucleotide sequence of TGB2 of said virus or its complementary cDNA, being operably linked to one or more regulatory sequence(s) active in a plant,
- transforming a plant cell with the nucleotide construct, and possibly
- regenerating a transgenic plant from the transformed plant cell.

2. Method according to the claim 1, characterised in that the nucleotide sequence of the nucleotide construct has at least 80% homology with the nucleotide sequence of TGB2 of said virus or its complementary cDNA.

Sub A1

3. Method according to the claim 1 or 2, characterised in that the group I virus is selected from the group consisting of hordéiviruses, benyviruses, pecluviruses and pomoviruses, preferably selected from the group consisting of the beet necrotic yellow vein virus, the barley stripe mosaic virus, the potato mop top virus, the peanut clump virus and the beet soil-borne virus.

4. Method according to any of the preceding claims, characterised in that the plant cell is a stomatal cell.

5. Method according to any of the preceding claims, characterised in that the plant is selected from the group consisting of sugar beet, potato, barley or peanut.

Sub A1 cont'd

6. Method according to claim 1 or 2, characterised in that the virus is BNYVV, the nucleotide sequence of TGB2 of said virus is comprised between the nucleotide 3287 and 3643 of the 5' strand of genomic or subgenomic RNA 2 of the BNYVV and the plant is a beet, preferably a sugar beet (*Beta vulgaris*).

7. Method according to any of the preceding claims, characterised in that the regulatory sequence comprises a promoter sequence or a terminator sequence active in a plant.

8. Method according to claim 7 characterised in that the promoter sequence is a constitutive or a foreigner promoter sequence.

9. Method according to the preceding claim 7, characterised in that the promoter sequence is selected from the group consisting of 35S Cauliflower Mosaic Virus promoter, and/or the polyubiquitin Arabidopsis thaliana promoter.

Sub A2

10. Method according to any of the claim 7 to 9, characterised in that the promoter sequence is a promoter which is capable of being active mainly into the root tissues of plants, such as the par promoter of the haemoglobin gene from Perosponia andersonii.

11. Transgenic plant resistant to a group I virus comprising a nucleotide construct having at least 70% homology with the nucleotide sequence of TGB2 of said virus or its corresponding cDNA, being operably linked to one or more regulatory sequence(s) active in a plant.

12. Transgenic plant according to the claim 11, characterised in that the nucleotide construct has a

nucleotide sequence corresponding to at least 80% homology with the nucleotide sequence of TGB2 of said virus or its complementary cDNA.

Sub A37

13. Transgenic plant according to the claim 11 or 12, characterised in that the virus is selected from the group consisting of hordéiviruses, benyviruses, pecluviruses and pomoviruses, preferably selected from the group consisting of the beet necrotic yellow vein virus, the barley stripe mosaic virus, the potato mop top virus, the peanut clump virus and the beet soil-borne virus.

14. Transgenic plant according to the claims 11 to 13 being a plant selected from the group consisting of sugar beet, potato, barley or peanut.

15. Transgenic plant according to the claims 11 or 12, characterised in that the transgenic plant being a beet, preferably a sugar beet (*Beta vulgaris*) the virus is BNYVV and the nucleotide sequence of TGB2 of said virus is comprised between the nucleotides 3287 and 3643 of the 5' strand of genomic or subgenomic RNA 2 of BNYVV or its corresponding cDNA.

16. Transgenic plant according to any of the preceding claims 11 to 15, characterised in that the regulatory sequence comprises a promoter sequence and a terminator sequence active in a plant.

17. Transgenic plant according to any of the preceding claims 11 to 16, characterised in that the regulatory sequence(s) comprise a promoter sequence which is a constitutive or a foreign promoter sequence.

18. Transgenic plant according to the claim 17, characterised in that promoter sequence is selected from the group consisting of 35S Cauliflower Mosaic Virus promoter, and/or the polyubiquitin *Arabidopsis thaliana* promoter.

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Sub A.4

19. Transgenic plant according to claim 17 or 18 characterised in that the promoter sequence is a promoter which is capable of being active mainly into root tissues, such as the *par* promoter of the haemoglobin gene from *Perosponia andersonii*.

20. Transgenic plant according to any one of the claims 11 to 19, characterised in that it further carries natural tolerance to Group I viruses.

21. Transgenic plant according to any one of the claims 11 to 20, characterised in that it further comprises a pesticide, herbicide or fungicide resistance, preferably a resistance selected from the group consisting of nematode resistance, glyphosate resistance, glufosomate resistance and/or acetochloride resistance.

22. Transgenic plant tissue selected from the group consisting of fruit, stem, root, tuber, seed of a plant according to any of the claims 11 to 21.